

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/552,552
Source: PCT/10
Date Processed by STIC: 10/20/05

ENTERED



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/552,552

DATE: 10/20/2005
TIME: 09:43:22

Input Set : N:\RJAVED\10552552.txt
Output Set: N:\CRF4\10202005\J552552.raw

3 <110> APPLICANT: Bayer BioScience N.V.
4 De Block, Marc
6 <120> TITLE OF INVENTION: Methods and means for increasing the tolerance of plants to
stress
7 conditions.
9 <130> FILE REFERENCE: BCS 03 2002 WO1
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/552,552
C--> 11 <141> CURRENT FILING DATE: 2005-10-07
11 <150> PRIOR APPLICATION NUMBER: EP03076044.1
12 <151> PRIOR FILING DATE: 2003-04-09
14 <150> PRIOR APPLICATION NUMBER: US 60/496,688
15 <151> PRIOR FILING DATE: 2003-08-21
17 <160> NUMBER OF SEQ ID NOS: 25
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 548
23 <212> TYPE: PRT
24 <213> ORGANISM: Arabidopsis thaliana
26 <400> SEQUENCE: 1
28 Met Glu Asn Arg Glu Asp Leu Asn Ser Ile Leu Pro Tyr Leu Pro Leu
29 1 5 10 15
32 Val Ile Arg Ser Ser Ser Leu Tyr Trp Pro Pro Arg Val Val Glu Ala
33 20 25 30
36 Leu Lys Ala Met Ser Glu Gly Pro Ser His Ser Gln Val Asp Ser Gly
37 35 40 45
40 Glu Val Leu Arg Gln Ala Ile Phe Asp Met Arg Arg Ser Leu Ser Phe
41 50 55 60
44 Ser Thr Leu Glu Pro Ser Ala Ser Asn Gly Tyr Ala Phe Leu Phe Asp
45 65 70 75 80
48 Glu Leu Ile Asp Glu Lys Glu Ser Lys Arg Trp Phe Asp Glu Ile Ile
49 85 90 95
52 Pro Ala Leu Ala Ser Leu Leu Gln Phe Pro Ser Leu Leu Glu Val
53 100 105 110
56 His Phe Gln Asn Ala Asp Asn Ile Val Ser Gly Ile Lys Thr Gly Leu
57 115 120 125
60 Arg Leu Leu Asn Ser Gln Gln Ala Gly Ile Val Phe Leu Ser Gln Glu
61 130 135 140
64 Leu Ile Gly Ala Leu Leu Ala Cys Ser Phe Phe Cys Leu Phe Pro Asp
65 145 150 155 160
68 Asp Asn Arg Gly Ala Lys His Leu Pro Val Ile Asn Phe Asp His Leu
69 165 170 175
72 Phe Ala Ser Leu Tyr Ile Ser Tyr Ser Gln Ser Gln Glu Ser Lys Ile
73 180 185 190
76 Arg Cys Ile Met His Tyr Phe Glu Arg Phe Cys Ser Cys Val Pro Ile

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77	195	200	205
80	Gly Ile Val Ser Phe Glu Arg Lys Ile Thr Ala Ala Pro Asp Ala Asp		
81	210	215	220
84	Phe Trp Ser Lys Ser Asp Val Ser Leu Cys Ala Phe Lys Val His Ser		
85	225	230	235
88	Phe Gly Leu Ile Glu Asp Gln Pro Asp Asn Ala Leu Glu Val Asp Phe		240
89	245	250	255
92	Ala Asn Lys Tyr Leu Gly Gly Ser Leu Ser Arg Gly Cys Val Gln		
93	260	265	270
96	Glu Glu Ile Arg Phe Met Ile Asn Pro Glu Leu Ile Ala Gly Met Leu		
97	275	280	285
100	Phe Leu Pro Arg Met Asp Asp Asn Glu Ala Ile Glu Ile Val Gly Ala		
101	290	295	300
104	Glu Arg Phe Ser Cys Tyr Thr Gly Tyr Ala Ser Ser Phe Arg Phe Ala		
105	305	310	315
108	Gly Glu Tyr Ile Asp Lys Lys Ala Met Asp Pro Phe Lys Arg Arg Arg		320
109	325	330	335
112	Thr Arg Ile Val Ala Ile Asp Ala Leu Cys Thr Pro Lys Met Arg His		
113	340	345	350
116	Phe Lys Asp Ile Cys Leu Leu Arg Glu Ile Asn Lys Ala Leu Cys Gly		
117	355	360	365
120	Phe Leu Asn Cys Ser Lys Ala Trp Glu His Gln Asn Ile Phe Met Asp		
121	370	375	380
124	Glu Gly Asp Asn Glu Ile Gln Leu Val Arg Asn Gly Arg Asp Ser Gly		
125	385	390	395
128	Leu Leu Arg Thr Glu Thr Thr Ala Ser His Arg Thr Pro Leu Asn Asp		400
129	405	410	415
132	Val Glu Met Asn Arg Glu Lys Pro Ala Asn Asn Leu Ile Arg Asp Phe		
133	420	425	430
136	Tyr Val Glu Gly Val Asp Asn Glu Asp His Glu Asp Asp Gly Val Ala		
137	435	440	445
140	Thr Gly Asn Trp Gly Cys Gly Val Phe Gly Gly Asp Pro Glu Leu Lys		
141	450	455	460
144	Ala Thr Ile Gln Trp Leu Ala Ala Ser Gln Thr Arg Arg Pro Phe Ile		
145	465	470	475
148	Ser Tyr Tyr Thr Phe Gly Val Glu Ala Leu Arg Asn Leu Asp Gln Val		480
149	485	490	495
152	Thr Lys Trp Ile Leu Ser His Lys Trp Thr Val Gly Asp Leu Trp Asn		
153	500	505	510
156	Met Met Leu Glu Tyr Ser Ala Gln Arg Leu Tyr Lys Gln Thr Ser Val		
157	515	520	525
160	Gly Phe Phe Ser Trp Leu Leu Pro Ser Leu Ala Thr Thr Asn Lys Ala		
161	530	535	540
164	Ile Gln Pro Pro		
165	545		
168	<210> SEQ ID NO: 2		
169	<211> LENGTH: 169		
170	<212> TYPE: PRT		
171	<213> ORGANISM: Solanum tuberosum		

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173 <400> SEQUENCE: 2
 175 Met Glu Asn Arg Glu Asp Val Lys Ser Ile Leu Pro Phe Leu Pro Val
 176 1 5 10 15
 179 Cys Leu Arg Ser Ser Ser Leu Phe Trp Pro Pro Leu Val Val Glu Ala
 180 20 25 30
 183 Leu Lys Ala Leu Ser Glu Gly Pro His Tyr Ser Asn Val Asn Ser Gly
 184 35 40 45
 187 Gln Val Leu Phe Leu Ala Ile Ser Asp Ile Arg Asn Ser Leu Ser Leu
 188 50 55 60
 191 Pro Asp Ser Ser Ile Ser Ser Ala Ser Asp Gly Phe Ser Leu Leu
 192 65 70 75 80
 195 Phe Asp Asp Leu Ile Pro Arg Asp Glu Ala Val Lys Trp Phe Lys Glu
 196 85 90 95
 199 Val Val Pro Lys Met Ala Asp Leu Leu Leu Arg Leu Pro Ser Leu Leu
 200 100 105 110
 203 Glu Ala His Tyr Glu Lys Ala Asp Gly Gly Ile Val Lys Gly Val Asn
 204 115 120 125
 207 Thr Gly Leu Arg Leu Leu Glu Ser Gln Gln Pro Gly Ile Val Phe Leu
 208 130 135 140
 211 Ser Gln Glu Leu Val Gly Ala Leu Leu Ala Cys Ser Phe Phe Cys Tyr
 212 145 150 155 160
 215 Ser Leu Pro Met Ile Glu Val Ser Val
 216 165
 219 <210> SEQ ID NO: 3
 220 <211> LENGTH: 1647
 221 <212> TYPE: DNA
 222 <213> ORGANISM: Arabidopsis thaliana
 224 <400> SEQUENCE: 3
 225 atggagaatc gcgaagatct taactcaatt cttccgtacc ttccacttgt aattcggtcg 60
 227 tcgtcgctgt attggccgccc gcgtgtggtg gaggcgtaa aggcaatgc tgaaggacca 120
 229 tctcacagcc aagtgtactc aggagagggtt ctacggcaag ctatttcga tatgagacga 180
 231 tccttatctt tctctactct cgagccatct gcttctaatg gctacgcatt tctctttgac 240
 233 gaatttattt atgagaaaaga atcaaagaga tggttcgatg agattatccc agcattggcg 300
 235 agcttacttc tacagtttcc atctctgtta gaagtgcatt tccaaaatgc tgataatatt 360
 237 gtagtgaa tcaaaaacgg tcttcgtttt ttaaattccc aacaagctgg cattgttttc 420
 239 ctcagccagg agttgattgg agcttcttgc gcatgctttt tctttttt gttccggat 480
 241 gataatagag gtgcaaaaaca cttccagtc atcaactttt atcatttttt tgcaaggcctt 540
 243 tatataagtt atagtcaaag tcaagaaaagc aagataagat gtattatgc ttactttgaa 600
 245 aggtttgtt cctgcgtgcc tattggattt gtttcattttt aacgcggat taccgctgtt 660
 247 cctgatgtt atttctggag caagtctgac gtttctttt gtgcattttt gggttcaactt 720
 249 ttgggtttaa ttgaagatca acctgacaat gctctcgaa tggacttgc aaacaaggat 780
 251 ctcggagggtt gttccctaag tagagggtgc gtgcaggaaag agatacgtt catgatataac 840
 253 cctgaattaa tcgctggcat gctttcttgc cctcgatgg atgacaatga agctatagaa 900
 255 atagttgggtt cggaaaagatt ttcatgttac acagggtatg catcttcgtt tcggtttgtt 960
 257 ggtgagtaca ttgacaaaaaa ggcaatggat ccttcaaaaaa ggcgaagaac cagaattttt 1020
 259 gcaattgtatg cattatgtac accgaagatg agacacttta aagatataatg tcttttaagg 1080
 261 gaaattaata aggcaactatg tggctttta aattttagca aggcttggga gcaccagaat 1140
 263 atattcatgg atgaaggaga taatgaaaatt cagttgtcc gaaacggcag agattctggt 1200
 265 cttctgcgtt cagaaactac tgcgtcacac cgaactccac taaaatgtt tgagatgaat 1260

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267	agagaaaagc	ctgctaaca	tcttacaga	gattttatg	tggaaggagt	tgataacgag	1320
269	gatcatgaag	atgatgggt	cgcgacaggg	aattggggat	gtggtgttt	tggaggagac	1380
271	ccagagctaa	aggctacgt	acaatggctt	gctgctccc	agactcgaag	accattata	1440
273	tcatattaca	ccttggagt	agaggcactc	cgaaacctag	atcaggtgac	gaagtggatt	1500
275	cttcccaata	aatggactgt	tggagatctg	tggaacatga	tgttagaata	ttctgctcaa	1560
277	aggctctaca	agcaaaccag	tgttggctc	ttttcttggc	tacttccatc	tctagctacc	1620
279	accaacaaag	ctatccagcc	gccttga				1647
282	<210>	SEQ ID NO:	4				
283	<211>	LENGTH:	598				
284	<212>	TYPE:	DNA				
285	<213>	ORGANISM:	Solanum tuberosum				
287	<400>	SEQUENCE:	4				
288	gcaatggaga	atagagaaga	cgtgaagtca	atccttcct	ttttgccgg	gtgtctccga	60
290	tcatcttctc	ttttctggcc	gccgctagtt	gttgaagcac	tgaaagccct	ctctgaaggc	120
292	cctcattaca	gcaatgttaa	ctccggccaa	gtcctcttcc	tcgcaatctc	cgacattcgg	180
294	aattcccttt	cactacctga	ttcttcaatt	tccttctctg	cttcagacgg	attttctctc	240
296	ttatattgatg	attnaattcc	tagggatgaa	gctgttaat	ggttcaaaga	agtggtgccg	300
298	aaaatggcgg	atttgctatt	gcgggtgcct	tccttattgg	aggctacta	tgagaaggct	360
300	gatggtgaaa	ttgttaaagg	agtcaacact	ggtcttcgct	tattggaatc	acaacagcct	420
302	ggcattgttt	tcctcagtca	ggaattagtc	ggtgtcttc	ttgcatgttc	cttctttgc	480
304	tattccctac	caatgataga	ggtatctgt	tgatcagtat	gacgagaaat	ttgaaaataa	540
306	attgaagtgc	atttctcaact	attttgagag	gattggctca	ttgataacctg	cgggctac	598
309	<210>	SEQ ID NO:	5				
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311	<212>	TYPE:	DNA				
312	<213>	ORGANISM:	Artificial Sequence				
314	<220>	FEATURE:					
315	<223>	OTHER INFORMATION:	oligonucleotide primer ParGAt1				
317	<400>	SEQUENCE:	5				
318	ggatcccctg	caggacaaaa	aggcaatgga	tcctttc			37
321	<210>	SEQ ID NO:	6				
322	<211>	LENGTH:	39				
323	<212>	TYPE:	DNA				
324	<213>	ORGANISM:	Artificial Sequence				
326	<220>	FEATURE:					
327	<223>	OTHER INFORMATION:	oligonucleotide primer ParGAt2				
329	<400>	SEQUENCE:	6				
330	gcacgaattc	gcggccgcgg	tgctcccaag	ccttgctac			39
333	<210>	SEQ ID NO:	7				
334	<211>	LENGTH:	39				
335	<212>	TYPE:	DNA				
336	<213>	ORGANISM:	Artificial Sequence				
338	<220>	FEATURE:					
339	<223>	OTHER INFORMATION:	oligonucleotide primer ParGST1				
341	<400>	SEQUENCE:	7				
342	ggatcccctg	caggctca	atgagaaggc	tgatggtgg			39
345	<210>	SEQ ID NO:	8				
346	<211>	LENGTH:	43				
347	<212>	TYPE:	DNA				

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Input Set : N:\RJAVED\10552552.txt
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348 <213> ORGANISM: Artificial Sequence
350 <220> FEATURE:
351 <223> OTHER INFORMATION: oligonucleotide primer ParGSt2
353 <400> SEQUENCE: 8
354 gcacgaattc gcggccgcgt catactgatc atacagatac ctc 43
357 <210> SEQ ID NO: 9
358 <211> LENGTH: 13466
359 <212> TYPE: DNA
360 <213> ORGANISM: Artificial Sequence
362 <220> FEATURE:
363 <223> OTHER INFORMATION: nucleotide sequence of pTVE428
365 <220> FEATURE:
366 <221> NAME/KEY: misc_feature
367 <222> LOCATION: (198)..(222)
368 <223> OTHER INFORMATION: Right T-DNA border
371 <220> FEATURE:
372 <221> NAME/KEY: misc_feature
373 <222> LOCATION: (983)..(273)
374 <223> OTHER INFORMATION: 3' ocs (3' untranslated end of octopine synthase gene)
377 <220> FEATURE:
378 <221> NAME/KEY: misc_feature
379 <222> LOCATION: (995)..(1155)
380 <223> OTHER INFORMATION: part of poly (ADP-ribose) glycohydrolase
383 <220> FEATURE:
384 <221> NAME/KEY: misc_feature
385 <222> LOCATION: (1929)..(1188)
386 <223> OTHER INFORMATION: intron 2 from the Pdk gene of Flaveria
389 <220> FEATURE:
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391 <222> LOCATION: (2122)..(1962)
392 <223> OTHER INFORMATION: part of poly (ADP-ribose) glycohydrolase
395 <220> FEATURE:
396 <221> NAME/KEY: misc_feature
397 <222> LOCATION: (3476)..(2131)
398 <223> OTHER INFORMATION: 35S promoter region from Cauliflower Mosaic Virus
401 <220> FEATURE:
402 <221> NAME/KEY: misc_feature
403 <222> LOCATION: (3948)..(3737)
404 <223> OTHER INFORMATION: 3' untranslated end of gene 7 from Agrobacterium tumefaciens
407 <220> FEATURE:
408 <221> NAME/KEY: misc_feature
409 <222> LOCATION: (4521)..(3970)
410 <223> OTHER INFORMATION: bar coding region
413 <220> FEATURE:
414 <221> NAME/KEY: misc_feature
415 <222> LOCATION: (6247)..(4522)
416 <223> OTHER INFORMATION: PSSuAra promoter region
419 <220> FEATURE:
420 <221> NAME/KEY: misc_feature

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/20/2005
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; Xaa Pos. 2,8,9,10,14,15,16,17,19,27,28,29
Seq#:11; Xaa Pos. 3,10,13,14,17,18,19
Seq#:12; Xaa Pos. 2,3,4,6,7,8,9
Seq#:13; Xaa Pos. 3,4,7,8
Seq#:14; Xaa Pos. 2,3,4,5,7
Seq#:21; N Pos. 18

VERIFICATION SUMMARY

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Input Set : N:\RJAVED\10552552.txt
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:917 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
M:341 Repeated in SeqNo=10
L:959 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
M:341 Repeated in SeqNo=11
L:989 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:1015 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:1041 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:1056 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:1053
L:1384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0